



# SEQUENCE LISTING

<110> MA, Jing  
GUO, Yajun

<120> PREPARATION AND APPLICATION OF  
ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

<130> 047630-0301

<140> US 10/723,003

<141> 2003-11-26

<150> CN 2003101199300

<151> 2003-11-25

<150> CN 031292909

<151> 2003-06-13

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 546

<212> DNA

<213> Homo sapiens

<400> 1

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546
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<210> 2

<211> 182

<212> PRT

<213> Homo sapiens

<400> 2

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Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
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Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
	50					55					60				
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
65					70					75					80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
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Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
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Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
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Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
	130					135					140				
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
145					150					155					160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
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Thr	Ala	Pro	Thr	Ala	Pro										
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<210> 3

<211> 1242

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 3

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120
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180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgtc ggggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga cctccgagca gctgggtggc
420
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480
gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca
540
gccccggagc ccaaattctg tgacaaaact cacacatgcc caccgtgcc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgate
660

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 780  
 gagcagtaca acagcacgta cggggtggtc tgcgtcctca ccgtcctgca ccaggactgg  
 840  
 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag  
 900  
 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca  
 960  
 tccccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat  
 1020  
 cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc  
 1080  
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 1140  
 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac  
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 1242

<210> 4  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 4  
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 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
 35 40 45  
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
 50 55 60  
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
 65 70 75 80  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
 85 90 95  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
 100 105 110  
 Phe Gln Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
 115 120 125  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
 130 135 140  
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
 145 150 155 160  
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala  
 165 170 175  
 Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 180 185 190  
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 195 200 205  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

210	215	220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val		
225	230	235
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr		240
	245	250
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val		255
	260	265
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys		270
	275	280
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser		285
	290	295
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro		300
305	310	315
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val		320
	325	330
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly		335
	340	345
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp		350
	355	360
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp		365
	370	375
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His		380
385	390	395
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		400
	405	410

<210> 5  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 5  
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<210> 6  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 6  
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<210> 7  
 <211> 426  
 <212> DNA  
 <213> Mus musculus

<400> 7  
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120  
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg  
180  
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc  
240  
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc  
300  
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc  
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420  
tcctca  
426

<210> 8  
<211> 138  
<212> PRT  
<213> Mus musculus

<400> 8  
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Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
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Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu  
50 55 60  
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
65 70 75 80  
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser  
85 90 95  
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val  
100 105 110  
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp  
115 120 125  
Gly Ala Gly Thr Thr Val Thr Val Ser Ser  
130 135

<210> 9  
<211> 465  
<212> DNA  
<213> Mus musculus

<400> 9  
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120  
tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaaag  
180

gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaataca gaagaactac  
 240  
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 300  
 actaggaat ctgggtgtccc tgatcgcttc acaggcagtg gatctgggac agattttact  
 360  
 cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc  
 420  
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 465

<210> 10  
 <211> 133  
 <212> PRT  
 <213> Mus musculus

<400> 10  
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 20 25 30  
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
 35 40 45  
 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60  
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80  
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
 100 105 110  
 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys  
 115 120 125  
 Leu Glu Ile Lys Arg  
 130

<210> 11  
 <211> 2021  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 11  
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 gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg  
 180  
 aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc  
 240  
 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc  
 300

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 360  
 tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc  
 420  
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 660  
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 780  
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 840  
 ttcacccgga gcctctgccc gcccactca tgctcaggga gagggctctc tggttttttc  
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 1080  
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 1320  
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 1620  
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 1680  
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 1860  
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 1920  
 gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc  
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actacacgca gaagagcctc tccctgtctc ccggtaaata g a  
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<210> 12

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

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			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35				40					45				
Thr	Ser	Tyr	Val	Met	His	Trp	Val	Lys	Gln	Lys	Pro	Gly	Gln	Gly	Leu
	50				55						60				
Asp	Trp	Ile	Gly	Tyr	Ile	Val	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn
65					70				75					80	
Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ser	Asp	Lys	Ser	Ser	Ser
			85					90					95		
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Val	Tyr	Gly	Ser	Arg	Tyr	Asp	Trp	Tyr	Leu	Asp	Val	Trp
		115				120						125			
Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
	130					135					140				
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
145					150					155					160
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
			165					170						175	
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			180					185					190		
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
		195					200					205			
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	210				215							220			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
225					230					235					240
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
			245						250					255	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			260					265					270		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		275					280						285		
His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly	Val	Glu
	290					295					300				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
305					310					315					320
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
			325						330					335	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
		340						345					350		
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln



	355		360		365										
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
	370					375						380			
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
385					390					395					400
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
				405					410					415	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
			420					425					430		
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
	435						440					445			
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
	450					455					460				
Ser	Pro	Gly	Lys												
465															

<210> 13  
 <211> 786  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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 120  
 tgtggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag  
 180  
 gtcactatga gctgtaagtc cagtcaaagt gttttatata gttcaaata gaagaactac  
 240  
 ttggcctggg accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc  
 300  
 actaggaat ctggtgtccc tgatecgttc acaggcagtg gatctgggac agattttact  
 360  
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 420  
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 480  
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 660  
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<210> 14  
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<212> PRT  
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<220>  
 <223> Synthetic Construct

<400> 14  
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 20 25 30  
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
 35 40 45  
 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60  
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80  
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
 100 105 110  
 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys  
 115 120 125  
 Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
 130 135 140  
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
 145 150 155 160  
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
 165 170 175  
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 180 185 190  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 195 200 205  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
 210 215 220  
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 15  
 <211> 426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 15  
 agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt  
 60  
 gtccactccc aggtgcagct ggtgcagctc gccggtggag tgggccagcc cggccgcagc  
 120  
 ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg  
 180  
 cgccaagccc ccggaaggc cctcgaatgg attggctaca ttgtgcctta taatgacggt  
 240

actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca  
 300  
 accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg  
 360  
 cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc  
 420  
 tcctct  
 426

<210> 16  
 <211> 138  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 16  
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly  
 1 5 10 15  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln  
 20 25 30  
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser  
 85 90 95  
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp  
 115 120 125  
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
 130 135

<210> 17  
 <211> 465  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 17  
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 60  
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 120  
 agaggaaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc  
 180  
 gtaacgatca cttgcaaata ctctcagtca gtattgtact ccagcaacca gaagaactac  
 240  
 ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc  
 300

acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg  
 360  
 ttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt  
 420  
 agttcctaca cttttggcca gggaactaaa ctgcagatta ctcga  
 465

<210> 18  
 <211> 135  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 18  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser  
 20 25 30  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser  
 35 40 45  
 Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr  
 50 55 60  
 Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser  
 65 70 75 80  
 Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
 85 90 95  
 Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala  
 100 105 110  
 Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly  
 115 120 125  
 Thr Lys Leu Gln Ile Thr Arg  
 130 135

<210> 19  
 <211> 2021  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 19  
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 gtccactccc aggtgcagct ggtgcagtct ggcggtggag tgggtccagcc cggccgcagc  
 120  
 ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg  
 180  
 cgccaagccc ccggaaggc cctcgaatgg attggctaca ttgtgcctta taatgacggt  
 240  
 actaagtaca atgaaaagtt caagggcaga ttacaatat caagtgaaa gagcaagtca  
 300  
 accgcattcc tccaaatgga cagcttgctt ccagaggaca ccgccgtata ctattgtgtg  
 360

cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc  
 420  
 tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc  
 480  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  
 540  
 gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttccccgc tgtctacag  
 600  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  
 660  
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt  
 720  
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 780  
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 840  
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 900  
 ccaggctctg ggcaggcaca ggctaggtgc ccctaaccga gccctgcac acaaaggggc  
 960  
 aggtgctggg ctgagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaa  
 1020  
 cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctccagat  
 1080  
 tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg  
 1140  
 cccaccgtgc ccaggtaagc cagcccaggc ctgcacctcc agtcaaggc gggacagggtg  
 1200  
 ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca  
 1260  
 tctcttctc agcacctgaa ctctggggg gaccgtcagt ctctctctc ccccaaaaac  
 1320  
 ccaaggacac cctcatgatc tcccggaccc ctgagggtcac atgctgggtg gtggacgtga  
 1380  
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg  
 1440  
 ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtctca  
 1500  
 ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag  
 1560  
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtg  
 1620  
 gagggccaca tggacagagg ccggctcggc ccacctctg ccctgagagt gaccgtgta  
 1680  
 ccaacctctg tctacaggg cagccccgag aaccacaggt gtacacctg ccccatccc  
 1740  
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca  
 1800  
 gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc  
 1860  
 ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga  
 1920  
 gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc  
 1980  
 actacgcga gaagagcctc tccctgtctc ccggtaaatg a  
 2021

<210> 20  
 <211> 468  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 20  
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly  
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 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln  
 20 25 30  
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser  
 85 90 95  
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp  
 115 120 125  
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro  
 130 135 140  
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
 145 150 155 160  
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
 165 170 175  
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
 180 185 190  
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
 195 200 205  
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn  
 210 215 220  
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser  
 225 230 235 240  
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
 245 250 255  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 260 265 270  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 275 280 285  
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu  
 290 295 300  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 305 310 315 320  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 325 330 335  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 340 345 350  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 355 360 365  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
385 390 395 400  
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
405 410 415  
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
420 425 430  
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
435 440 445  
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
450 455 460  
Ser Pro Gly Lys  
465

<210> 21  
<211> 786  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 21  
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120  
agaggaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc  
180  
gtaacgatca cttgcaaata ctctcagtcga gtattgtact ccagcaacca gaagaactac  
240  
ctggccggat atcagcagac tcccggcaaa gcccacaaagt tgctgattta ttgggcctcc  
300  
acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg  
360  
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420  
agttcctaca cttttggcca gggaaactaaa ctgcagatta ctggaactgt ggctgcacca  
480  
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg  
540  
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc  
600  
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac  
660  
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc  
720  
tgcgaagtca cccatcaggg cctgagctcg cccgtcacia agagcttcaa caggggagag  
780  
tgtag  
786

<210> 22  
<211> 241  
<212> PRT  
<213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 22  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser  
 20 25 30  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser  
 35 40 45  
 Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr  
 50 55 60  
 Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser  
 65 70 75 80  
 Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
 85 90 95  
 Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala  
 100 105 110  
 Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly  
 115 120 125  
 Thr Lys Leu Gln Ile Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile  
 130 135 140  
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val  
 145 150 155 160  
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys  
 165 170 175  
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu  
 180 185 190  
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu  
 195 200 205  
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 210 215 220  
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
 225 230 235 240  
 Cys

<210> 23  
 <211> 2489  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 23  
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 60  
 gtccactccc aggtgcagct ggtgcagtct ggcggtggag tgggtccagcc cggccgcagc  
 120  
 ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg  
 180  
 cgccaagccc ccggaaggc cctcgaatgg attggctaca ttgtgcctta taatgacggt  
 240  
 actaagtaca atgaaaagtt caagggcaga ttacaatat caagtgacaa gagcaagtca  
 300



accgcattcc tccaaatgga cagcttgcggt ccagaggaca ccgccgtata ctattgtgtg  
 360  
 cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc  
 420  
 tcctctgcta gcaccaaggg cccatcggtc tccccctgg caccctctc caagagcacc  
 480  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  
 540  
 gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag  
 600  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  
 660  
 cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt  
 720  
 ggtgagaggc cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc  
 780  
 tggacgcatt ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc  
 840  
 ttcacccgga gcctctgccc gcccactca tgctcaggga gaggtcttc tggctttttc  
 900  
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 960  
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 1020  
 cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat  
 1080  
 tccagtaact cccaatcttc tctctgcaga gccc aaatct tgtgacaaaa ctacacatg  
 1140  
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 1200  
 ccctagagta gcctgcatcc agggacaggc ccagccggg tgctgacacg tccacctcca  
 1260  
 tctcttctc agcacctgaa ctctggggg gaccgtcagt ctctctctc cccccaaaac  
 1320  
 ccaaggacac cctcatgatt tcccggacct ctgaggtcac atgcgtgggtg gtggacgtga  
 1380  
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg  
 1440  
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 1500  
 ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag  
 1560  
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtg  
 1620  
 gagggccaca tggacagagg ccggctcggc ccacctctg ccctgagagt gaccgtgta  
 1680  
 ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacacctg ccccatccc  
 1740  
 gggatgagct gaccaagaac caggtcagcc tgacctgctt ggtcaaaggc ttctatccca  
 1800  
 gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc  
 1860  
 ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga  
 1920  
 gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc  
 1980

actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac  
2040  
acagcccat ctcctccgac ttcgtgtgca aaatccgtga gctgtctgac tacctgcttc  
2100  
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct  
2160  
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggccaaga  
2220  
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc  
2280  
agccccccc cagctgtctt cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga  
2340  
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc  
2400  
tgagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccgccccc  
2460  
tgaggccac agccccgaca gcccgtga  
2489

<210> 24  
<211> 624  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 24  
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly  
1 5 10 15  
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln  
20 25 30  
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60  
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
65 70 75 80  
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser  
85 90 95  
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val  
100 105 110  
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp  
115 120 125  
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro  
130 135 140  
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
145 150 155 160  
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
165 170 175  
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
180 185 190  
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
195 200 205  
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn  
210 215 220  
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser

225					230					235				240
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
				245					250					255
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
			260					265					270	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		275					280					285		
His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly	Val
	290					295					300			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
305					310					315				320
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
				325					330					335
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
			340					345					350	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
	355						360					365		
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln
	370					375					380			
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
385					390					395				400
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
				405					410					415
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
			420					425					430	
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
	435						440					445		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
	450					455					460			
Ser	Pro	Gly	Lys	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile
465					470					475				480
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu
				485					490					495
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu
			500					505					510	
Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg
		515					520					525		
Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val
	530					535					540			
Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro
545					550					555				560
Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu
				565					570					575
Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn
			580					585					590	
Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu
		595					600					605		
Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr	Ala
	610					615					620			

<210> 25  
 <211> 2534  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Synthetic Construct

<400> 25

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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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<210> 28  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
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 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
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 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
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 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
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 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser



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Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
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Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
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Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
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Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
		275				280						285			
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
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Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
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Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
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Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
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			405						410					415	
Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu
			420					425					430		
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 <211> 2489  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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<210> 30
<211> 624
<212> PRT
<213> Artificial Sequence

<220>

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<400> 30

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Ser	Pro	Gly	Lys	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
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Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
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Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys
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Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn
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Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser
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Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr
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Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe
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 <213> Artificial Sequence

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 <223> Synthetic Construct

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<210> 32

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 32

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Thr	Ser	Tyr	Val	Met	His	Trp	Val	Lys	Gln	Lys	Pro	Gly	Gln	Gly	Leu
	50				55					60					
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Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
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Tyr	Tyr	Cys	Val	Tyr	Gly	Ser	Arg	Tyr	Asp	Trp	Tyr	Leu	Asp	Val	Trp
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Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
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Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
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His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
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Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
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Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr

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Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
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Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
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Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
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Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
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Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
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Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
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Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
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			500					505					510		
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Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys
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Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr
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Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys
				565					570					575	
Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser
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<210> 33

<211> 1986

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 33

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<210> 34  
 <211> 661  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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 35 40 45  
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 50 55 60  
  
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 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
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 165 170 175  
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 180 185 190  
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 195 200 205  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
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 225 230 235 240  
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 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
 260 265 270  
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 275 280 285  
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<210> 36  
<211> 140  
<212> PRT  
<213> Mus musculus

<400> 36  
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50 55 60  
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn  
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Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
85 90 95  
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<210> 37  
<211> 390  
<212> DNA  
<213> Mus musculus

<400> 37  
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240  
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<210> 38  
 <211> 129  
 <212> PRT  
 <213> Mus musculus

<400> 38  
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 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro  
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 Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
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 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 115 120 125  
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<210> 39  
 <211> 2021  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 39  
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<210> 40

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

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Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
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Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn	
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Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
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Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	
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Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
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		260						265					270			
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
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Val	Ser	His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly	
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Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	
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Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
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Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	
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Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
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Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
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465					470										

<210> 41  
<211> 711

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

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<210> 42  
<211> 235  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 42  
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Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	
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Ser	Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser	
	50					55					60					
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	
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Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	
			85						90					95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	
			100					105					110			
Thr	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
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Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	
	130					135					140					
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	
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Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	
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Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
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Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	
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<210> 43  
 <211> 2489  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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 2489

<210> 44  
 <211> 626  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 44  
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 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu  
 50 55 60  
 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn  
 65 70 75 80  
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn  
 115 120 125  
 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys  
 130 135 140  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 145 150 155 160  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 165 170 175  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 180 185 190  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
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 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 210 215 220  
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 225 230 235 240  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
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<210> 46

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

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Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1          5          10          15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20          25          30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35          40          45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50          55          60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65          70          75          80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85          90          95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100          105          110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
115          120          125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys

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130	135	140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
145	150	155
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro		
	165	170
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr		
	180	185
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val		
	195	200
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn		
	210	215
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro		
225	230	235
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu		
	245	250
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp		
	260	265
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp		
	275	280
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly		
	290	295
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn		
305	310	315
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp		
	325	330
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro		
	340	345
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu		
	355	360
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn		
	370	375
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
385	390	395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr		
	405	410
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
	420	425
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
	435	440
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
450	455	460
Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
465	470	475
Gly Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile		
	485	490
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu		
	500	505
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu		
	515	520
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg		
	530	535
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val		
545	550	555
Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro		
	565	570
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu		
	575	

			580					585					590						
Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn				
		595					600					605							
Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	610					615					620								
Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr	Ala				
625					630					635					640				
Pro																			

<210> 47  
 <211> 1974  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 47  
 atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg  
 60  
 agctcgggac tcagtgggac ccaggactgc tccttccaac acagcccat ctcctccgac  
 120  
 ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg  
 180  
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag  
 240  
 cgctggatgg agcgggtcaa gactgtcgct gggccaaga tgcaaggctt gctggagcgc  
 300  
 gtgaacacgg agatacactt tgtcaccaaa tgtgccttc agccccccc cagctgtctt  
 360  
 cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga cctccgagca gctgggtggcg  
 420  
 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc  
 480  
 gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca  
 540  
 gccccggagc ccaaattctg tgacaaaact cacacatgcc caccgtgcc agcacctgaa  
 600  
 ctcttggggg gaccgtcagt ctctctcttc cccccaaaac ccaaggacac cctcatgac  
 660  
 tcccggaacc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc  
 720  
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag  
 780  
 gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg  
 840  
 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag  
 900  
 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca  
 960  
 tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggtttctat  
 1020  
 ccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc  
 1080



acgcctccccg tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac  
 1140  
 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac  
 1200  
 aaccactaca cgcagaagag cctctccctg tctcccggta aacaggtaca actacagcag  
 1260  
 cctggggctg agctggtgaa gcctggggcc tcagtgaaga tgtcctgcaa ggcttctggc  
 1320  
 tacacattta ccagttacaa tatgcaactgg gtaaagcaga cacctggtcg gggcctggaa  
 1380  
 tggattggag ctatttatcc aggaaatggg gatacttcct acaatcagaa gttcaagggc  
 1440  
 aaggccacac tgactgcaga caaatcctcc agcacagcct acatgcagct cagcagcctg  
 1500  
 acatctgaag actctgcggg ctattactgt gcaagatcga cttactacgg cggtgactgg  
 1560  
 tacttcaatg tctggggcgc agggaccacg gtcaccgtct ctgcaggcgg tggaggctct  
 1620  
 ggtggaggcg gttcaggagg cgggtgatct caaattgttc tctcccagtc tccagcaatc  
 1680  
 ctgtctgcat ctccagggga gaaggtcaca atgacttgca gggccagctc aagtgttaagt  
 1740  
 tacatccact gggtccagca gaagccagga tctccccca aaccctggat ttatgccaca  
 1800  
 tccaacctgg cttctggagt ccctgttcgc ttcagtggca gtgggtctgg gacctcttac  
 1860  
 tctctcacia tcagtagagt ggaggctgaa gatgctgcca cttattactg ccagcagtgg  
 1920  
 actagtaacc caccacggtt cgggtggtggg accaagctgg agatcaaacg atga  
 1974

<210> 48  
 <211> 657  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 48  
 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu  
 1 5 10 15  
 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe  
 20 25 30  
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
 35 40 45  
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
 50 55 60  
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
 65 70 75 80  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
 85 90 95  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
 100 105 110  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
 115 120 125  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp

130	135	140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro		
145	150	155
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala		160
	165	170
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr		175
	180	185
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe		190
	195	200
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro		205
	210	215
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val		220
225	230	235
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr		240
	245	250
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val		255
	260	265
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys		270
	275	280
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser		285
	290	295
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro		300
305	310	315
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val		320
	325	330
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly		335
	340	345
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp		350
	355	360
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp		365
	370	375
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His		380
385	390	395
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val		400
	405	410
Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val		415
	420	425
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met		430
	435	440
His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala		445
	450	455
Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly		460
465	470	475
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln		480
	485	490
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg		495
	500	505
Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly		510
	515	520
Thr Thr Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly		525
	530	535
Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile		540
545	550	555
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser		560
	565	570
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser		575
	580	585
		590

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
		595					600					605			
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
	610					615					620				
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
625					630					635					640
Thr	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
				645					650					655	

Arg

<210> 49  
 <211> 426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 49  
 atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc  
 60  
 agaggagagg ttcagctggg ggagctctggc ggtggcctgg tgcagccagg gggctcactc  
 120  
 cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt  
 180  
 caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact  
 240  
 agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca  
 300  
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga  
 360  
 tggggagggg acggcttcta tgctatggac tactgggggtc aaggaaccct ggtcaccgtc  
 420  
 tcctcg  
 426

<210> 50  
 <211> 142  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 50  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly  
 20 25 30  
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
 35 40 45  
 Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly  
 50 55 60  
 Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr  
 65 70 75 80

Arg	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr
				85					90					95	
Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
			100					105					110		
Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala
		115					120					125			
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
	130					135					140				

<210> 51

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 51

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atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc
60
agaggagaca tccagatgac ccagtcctccg agctccctgt ccgcctctgt gggcgatagg
120
gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag
180
aaaccaggaa aagctccgaa actactgatt tactcggcac ccttcctcta ctctggagtc
240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtcctg
300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc
360
ggacagggta ccaaggtgga gatcaaacgt
390

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<210> 52

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 52

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ser	Arg	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser
			20					25					30		
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Gln	Asp	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
	50					55				60					
Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val
65					70					75				80	
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
			85					90					95		
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln

		100						105						110
His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu Ile
		115					120					125		
Lys	Arg													
	130													

<210> 53  
 <211> 2021  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 53  
 atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc  
 60  
 agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc  
 120  
 cgtttgtcct gtgcagcttc tggtttcaac attaaagaca cctatataca ctgggtgcgt  
 180  
 caggcccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact  
 240  
 agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca  
 300  
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga  
 360  
 tggggagggg acggcttcta tgctatggac tactgggggtc aaggaaccct ggtcacctgc  
 420  
 tcctcggcta gcaccaaggg cccatcggtc tccccctgg caccctctc caagagcacc  
 480  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accgggtgacg  
 540  
 gtgtcttga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag  
 600  
 tcctcaggac tctactcct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  
 660  
 cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt  
 720  
 ggtgagaggc cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc  
 780  
 tggacgcac ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc  
 840  
 ttcacccgga gcctctgccc gcccactca tgctcaggga gagggctctc tggctttttc  
 900  
 ccaggctctg ggcaggcaca ggctaggtgc ccctaaccga ggccctgcac acaaaggggc  
 960  
 aggtgctggg ctacagactg ccaagagcca tatccgggag gaccctgccc ctgacctaa  
 1020  
 cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat  
 1080  
 tccagtaact cccaatcttc tctctgcaga gcccaaactt tgtgacaaaa ctcacacatg  
 1140  
 cccaccgtgc ccaggtaagc cagcccaggc ctgcacctcc agctcaaggc gggacagggtg  
 1200

ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca  
 1260  
 tctcttctc agcacctgaa ctcttggggg gaccgtcagt ctctctcttc cccccaaaac  
 1320  
 ccaaggacac cctcatgata tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga  
 1380  
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg  
 1440  
 ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca  
 1500  
 ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag  
 1560  
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtgc  
 1620  
 gagggccaca tggacagagg cgggctcggc ccaccctctg ccctgagagt gaccgctgta  
 1680  
 ccaacctctg tcttacaggg cagccccgag aaccacaggt gtacaccctg ccccatcccc  
 1740  
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca  
 1800  
 gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc  
 1860  
 ctcccgtgct ggactccgac ggctccttct tctctacag caagctcacc gtggacaaga  
 1920  
 gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc  
 1980  
 actacacgca gaagagcctc tccctgtctc ccggtaaatg a  
 2021

<210> 54

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

1	5	10	15
Val Ile Ile	Ser Arg Gly Glu Val	Gln Leu Val Glu Ser	Gly Gly Gly
	20	25	30
Leu Val Gln	Pro Gly Gly Ser	Leu Arg Leu Ser	Cys Ala Ala Ser Gly
	35	40	45
Phe Asn Ile	Lys Asp Thr Tyr Ile	His Trp Val Arg	Gln Ala Pro Gly
	50	55	60
Lys Gly Leu	Glu Trp Val Ala Arg	Ile Tyr Pro Thr	Asn Gly Tyr Thr
	65	70	75
Arg Tyr Ala	Asp Ser Val Lys Gly	Arg Phe Thr Ile	Ser Ala Asp Thr
	85	90	95
Ser Lys Asn	Thr Ala Tyr Leu Gln	Met Asn Ser Leu	Arg Ala Glu Asp
	100	105	110
Thr Ala Val	Tyr Tyr Cys Ser	Arg Trp Gly Gly	Asp Gly Phe Tyr Ala
	115	120	125
Met Asp Tyr	Trp Gly Gln Gly Thr	Leu Val Thr Val	Ser Ser Ala Ser
	130	135	140

Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	145	150	155	160
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	165	170	175	
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	180	185	190	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	195	200	205	
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	210	215	220	
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	225	230	235	240
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	245	250	255	
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	260	265	270	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	275	280	285	
Val	Asp	Val	Ser	His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	290	295	300	
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	305	310	315	320
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	325	330	335	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	340	345	350	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	355	360	365	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	370	375	380	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	385	390	395	400
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	405	410	415	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	420	425	430	
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	435	440	445	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	450	455	460	
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys									465	470		

<210> 55

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 55

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agaggagaca tccagatgac ccagtcctccg agctccctgt ccgcctctgt gggcgatagg  
120

gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag  
 180  
 aaaccaggaa aagctccgaa actactgatt tactcggcat ccttcctcta ctctggagtc  
 240  
 ccttctcgct tctctggctc cagatctggg acggatttca ctctgacat cagcagtcgt  
 300  
 cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc  
 360  
 ggacagggta ccaaggtgga gatcaaacgt actgtggctg caccatctgt cttcatcttc  
 420  
 ccgcatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac  
 480  
 ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac  
 540  
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc  
 600  
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat  
 660  
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 711

<210> 56  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 56  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
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 20 25 30  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45  
 Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60  
 Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val  
 65 70 75 80  
 Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr  
 85 90 95  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 115 120 125  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 130 135 140  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 145 150 155 160  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 165 170 175  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 180 185 190  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 195 200 205



Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
210						215					220				
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
225					230					235					

<210> 57  
 <211> 2489  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 57  
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 120  
 cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatatata ctgggtgcgt  
 180  
 caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact  
 240  
 agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca  
 300  
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga  
 360  
 tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcacctgc  
 420  
 tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc  
 480  
 tctgggggca cagcggccct gggtgcctg gtcaaggact acttccccga accggtgacg  
 540  
 gtgtcttggg actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag  
 600  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  
 660  
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 720  
 ggtgagaggg cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc  
 780  
 tggacgcac ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc  
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 960  
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 1020  
 cccaccccaa aggccaaact ctccactccc tcagctcggg caccttctct cctccagat  
 1080  
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 1140  
 cccaccgtgc ccaggtaagc cagcccaggc ctgcacctcc agctcaaggc gggacagggtg  
 1200  
 ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca  
 1260

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1320  
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1380  
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg  
1440  
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtgggtc tgcgtcctca  
1500  
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag  
1560  
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1620  
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1680  
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1800  
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc  
1860  
ctcccgctgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga  
1920  
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc  
1980  
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac  
2040  
acagcccat ctctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc  
2100  
aagattacc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct  
2160  
ggcggctggc cctggcacag cgtggtgatg agcggctcaa gactgtcgct ggggtccaaga  
2220  
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2280  
agccccccc cagctgtctt cgttctgtcc agaccaacat ctccgcctc ctgcaggaga  
2340  
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccgtgcc  
2400  
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2460  
tgagggccac agccccgaca gccccgtga  
2489

<210> 58

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 58

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
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Val	Ile	Ile	Ser	Arg	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly
			20					25					30		
Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly



				485					490					495	
Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp
			500					505					510		
Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp
		515					520					525			
Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu
	530					535					540				
Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln
545					550					555					560
Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu
			565						570					575	
Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr
			580					585					590		
Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser
		595					600					605			
Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala
	610					615					620				
Pro	Thr	Ala	Pro												
625															

<210> 59  
 <211> 2534  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 59  
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 120  
 cgtttgtcct gtgcagcttc tggtctcaac attaaagaca cctatataca ctgggtgcgt  
 180  
 caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact  
 240  
 agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca  
 300  
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga  
 360  
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 420  
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 480  
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 660  
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 720  
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 780

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 840  
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 960  
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 1020  
 cccaccccaa aggcacaaact ctccactccc tcagctcgga caccttctct cctcccagat  
 1080  
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 1260  
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 1800  
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 1860  
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 1920  
 gcagggtggc gcagggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc  
 1980  
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 2040  
 gcgggttcagg aggcgggtga tctaccagg actgctcctt ccaacacagc cccatctcct  
 2100  
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 2160  
 ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg  
 2220  
 cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg  
 2280  
 agcgcgtgaa cacggagata cactttgtca ccaaagtgtc ctttcagccc cccccagct  
 2340  
 gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctc gagcagctgg  
 2400  
 tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc  
 2460

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 2520  
 cgacagcccc gtga  
 2534

<210> 60  
 <211> 643  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 60  
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 1 5 10 15  
 Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly  
 20 25 30  
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
 35 40 45  
 Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly  
 50 55 60  
 Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr  
 65 70 75 80  
 Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr  
 85 90 95  
 Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 100 105 110  
 Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala  
 115 120 125  
 Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
 130 135 140  
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
 145 150 155 160  
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
 165 170 175  
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 180 185 190  
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser  
 195 200 205  
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
 210 215 220  
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
 225 230 235 240  
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
 245 250 255  
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
 260 265 270  
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 275 280 285  
 Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 290 295 300  
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 305 310 315 320  
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 325 330 335  
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala



gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag  
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 720  
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 1080  
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 1140  
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 1800  
 ccgaaactac tgatttactc ggcaccttc ctctactctg gagtcccttc tgccttctct  
 1860



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 1920  
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 1980  
 gtggagatca aacgttga  
 1998

<210> 62  
 <211> 665  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 62  
 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu  
 1 5 10 15  
 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe  
 20 25 30  
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
 35 40 45  
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
 50 55 60  
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
 65 70 75 80  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
 85 90 95  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
 100 105 110  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
 115 120 125  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
 130 135 140  
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
 145 150 155 160  
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala  
 165 170 175  
 Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 180 185 190  
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 195 200 205  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
 210 215 220  
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
 225 230 235 240  
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 245 250 255  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
 260 265 270  
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 275 280 285  
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 290 295 300  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 305 310 315 320

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 325 330 335  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 340 345 350  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 355 360 365  
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 370 375 380  
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 385 390 395 400  
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val  
 405 410 415  
 Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu  
 420 425 430  
 Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile  
 435 440 445  
 His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg  
 450 455 460  
 Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly  
 465 470 475 480  
 Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln  
 485 490 495  
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg  
 500 505 510  
 Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
 515 520 525  
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Gly Gly  
 530 535 540  
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln  
 545 550 555 560  
 Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
 565 570 575  
 Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp  
 580 585 590  
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala  
 595 600 605  
 Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser  
 610 615 620  
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe  
 625 630 635 640  
 Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly  
 645 650 655  
 Gln Gly Thr Lys Val Glu Ile Lys Arg  
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<210> 63

<211> 1098

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 63

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180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag
240
cgctggatgg agcgggtcaa gactgtcgct gggccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagca gctgggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
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660
tcttctccaa actccaagaa tgaaaaggct ctgggccgca aaataaactc ctgggaatca
720
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780
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840
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900
cctgacccta tattgttgat gaaaagtgc agaaatagtt gttggtctaa agatgcagaa
960
tatggactct attccatcta tcaaggggga atatttgagc ttaaggaaaa tgacagaatt
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1098

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<210> 64

<211> 365

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

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Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1          5          10          15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
          20          25          30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
          35          40          45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
          50          55          60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65          70          75          80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly

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gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt  
 360  
 cgcttcgtcc agaccaacat ctcccgccctc ctgcaggaga cctccgagca gctgggtggcg  
 420  
 ctgaagccct ggatcactcg ccagaacttc tcccgggtgcc tggagctgca gtgtcagccc  
 480  
 gactcctcaa ccctgccacc cccatggagt ccccggtccc tggaggccac agccccgaca  
 540  
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 600  
 gagaacgaga tcgcccggat taagaaactc attggcgaga cctctgagga aaccatttct  
 660  
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 720  
 gtagcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc  
 780  
 aagaatgaaa aggctctggg ccgcaaaaata aactcctggg aatcatcaag gagtgggcat  
 840  
 tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaaggggtt  
 900  
 tactacatct attcccaaac atactttcga tttcaggagg aaataaaaga aaacacaaag  
 960  
 aacgacaaac aaatgggtcca atatatattac aaatacaciaa gttatcctga ccctatatg  
 1020  
 ttgatgaaaa gtgctagaaa tagttgttgg tctaaagatg cagaatatgg actctattcc  
 1080  
 atctatcaag ggggaatatt tgagcttaag gaaaatgaca gaatttttgt ttctgtaaca  
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<210> 66  
 <211> 400  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 66  
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 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
 35 40 45  
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
 50 55 60  
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
 65 70 75 80  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
 85 90 95  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
 100 105 110  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser

	115		120		125									
Arg	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
	130				135					140				
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln
145					150					155				160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu
				165					170					175
Thr	Ala	Pro	Thr	Ala	Pro	Met	Lys	Gln	Ile	Glu	Asp	Lys	Ile	Glu
			180					185					190	
Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	Glu	Ile	Ala	Arg	Ile
	195						200					205		
Lys	Leu	Ile	Gly	Glu	Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln
	210					215					220			
Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln
225					230				235					240
Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu
			245					250						255
Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn
		260					265						270	
Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His
	275					280						285		
Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile
	290					295				300				
Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr
305					310					315				320
Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr
			325						330					335
Asp	Pro	Ile	Leu	Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys
		340					345					350		
Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe
	355					360					365			
Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His
	370					375				380				
Ile	Asp	Met	Asp	His	Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val
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<210> 67  
 <211> 1749  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 67  
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 180  
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag  
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 300

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420
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480
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540
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660
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720
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780
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960
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1020
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1080
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1140
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1260
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1320
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1380
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1440
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1500
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1560
atattgttga tgaaaagtgc tagaaatagt tgttggtcta aagatgcaga atatggactc
1620
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1749

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<210> 68

<211> 582

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 68

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Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe			
			20					25					30					
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu			
		35					40					45						
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu			
	50					55					60							
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln			
65					70					75					80			
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly			
			85						90					95				
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala			
			100					105					110					
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser			
		115					120					125						
Arg	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp				
	130					135					140							
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro			
145					150					155					160			
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala			
				165					170					175				
Thr	Ala	Pro	Thr	Ala	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr			
			180					185					190					
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe			
		195					200					205						
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro			
	210					215					220							
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val			
225					230					235					240			
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr			
				245					250					255				
Lys	Pro	Arg	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val				
			260				265					270						
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys			
		275				280						285						
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser			
	290					295					300							
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro			
305					310					315					320			
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val			
				325					330					335				
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly			
			340					345					350					
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp			
		355					360					365						
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp			
	370					375					380							
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His			
385					390					395					400			
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Val	Arg			
				405					410					415				
Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly			
			420					425					430					



Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu
		435					440					445			
Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	Phe
	450					455					460				
Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	Lys
465					470					475					480
Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu
				485					490					495	
Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr
			500					505					510		
Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	Ala	Arg
		515					520					525			
Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr
	530					535					540				
Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser
545					550					555					560
Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	Ser	Phe	Phe
				565					570					575	
Gly	Ala	Phe	Leu	Val	Gly										
			580												

<210> 69  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Primer

<400> 69  
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 31

<210> 70  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Primer

<400> 70  
 gagcccaaatt cttgtgacaa aac  
 23